JC20 Rec'd PCT/PTO 22 JUN 2005

SEQUENCE LISTING

<110> Geigenberger, Peter

<110.	La Vi St va	inger, igeolas itt Ni in Dong ivardi,	Anke , Hei gel, en, d	lene Maro Joost	2										
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Glu s		ggg cct Sly Pro													192
		gca ctg Ala Leu													240
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aag ctc aag cc Lys Leu Lys Pro 65					r
gca gta caa ct Ala Val Gln Le					
ttg aag aga ct Leu Lys Arg Le 10	u Gly Ala Ser				
cac ttt gag gt His Phe Glu Va 115					
gtg ccg gag at Val Pro Glu Me 130	g tgg tca ccg t Trp Ser Pro 135	gag atg aag Glu Met Lys	gtg gct tgg Val Ala Trp 140	ggt cag go Gly Gln Al	t 432 a
tat gat cac ct Tyr Asp His Let 145	t gtt gct gcc u Val Ala Ala 150	att aaa gct Ile Lys Ala	gaa atg aat Glu Met Asn 155	ctt tcc aa Leu Ser As 16	n
taa		483			

taa 483

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4b

gct cat gct Ala His Ala 65													240
ctg agg gag Leu Arg Glu													288
tta ggc tca Leu Gly Ser													336
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130 135 140



SEQUENCE LISTING

<110> Max-Planck-Gesellschaft

<120> Method for modifying the storage reserve content in plants

<130> NAE 737/02 PCT

<150> DE 10260707.9

<151> 2002-12-23

<160> 6

<170> PatentIn version 3.2

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<212> DNA

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aca ttc aag aaa aac ctt cct acc aac agt gtt ttg ttc tac acc gtt 96

Thr Phe Lys Lys Asn Leu Pro Thr Asn Ser Val Leu Phe Tyr Thr Val 20 25 30 ata ttg gag ata gca cca act gca aaa gac atg ttc tcc ttt cta aag 144

Ile Leu Glu Ile Ala Pro Thr Ala Lys Asp Met Phe Ser Phe Leu Lys 35 40 45

gag tot ggg cot aag cat agt cot cag ctc cag gcc cat gct gaa aag 192

Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys 50 55 60

gtt ttt gca ctg act cgt gat gct gcc act caa ctc gta gca aaa gga 240

Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly 65 70 75 80

gaa gtg aca ctt gca gat gcc agc tta ggt gct gtc cac gtt cag aaa 288

Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys 85 90 95

gcc gtt act gat cct cat ttc gtg gtg gtt aaa gaa gcc ctg ctt caa 336

Ala Val Thr Asp Pro His Phe Val Val Lys Glu Ala Leu Leu Gln
100 105 110

aca gta aag gaa gca gtt ggg gcg gac gaa tgg agt gat gac ttg agc 384

Thr Val Lys Glu Ala Val Gly Ala Asp Glu Trp Ser Asp Asp Leu Ser 115 120 125

acc gct tgg gaa gga gca tat gat gga cta gca act gca att aag aag 432

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gca atg ggt taa Ala Met Gly 145 444

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Ile Leu Glu Ile Ala Pro Thr Ala Lys Asp Met Phe Ser Phe Leu Lys 35 40 45

Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys
50 55 60

Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly 65 70 75 80

Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys 85 90 95 Ala Val Thr Asp Pro His Phe Val Val Lys Glu Ala Leu Leu Gln
100 105 110

Thr Val Lys Glu Ala Val Gly Ala Asp Glu Trp Ser Asp Asp Leu Ser 115 120 125

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Val Val Lys Ser Trp Ser Val Met Lys Lys Asn Ser Ala Glu Leu Gly
20 25 30

ctc aaa ctc ttc atc aag atc ttt gag att gca cca aca acg aag aag 144

Leu Lys Leu Phe Ile Lys Ile Phe Glu Ile Ala Pro Thr Thr Lys Lys
35 40 45

atg ttc tct ttc ttg aga gac tca cca att cct gct gag caa aat cca 192

Met Phe Ser Phe Leu Arg Asp Ser Pro Ile Pro Ala Glu Gln Asn Pro 50 55 60

aag ctc aag cct cac gca atg tct gtt ttt gtc atg tgt tgt gaa tca 240

Lys Leu Lys Pro His Ala Met Ser Val Phe Val Met Cys Cys Glu Ser 65 70 75 80

gca gta caa ctg agg aaa aca ggg aaa gtt acg gtg agg gag act act 288

Ala Val Gln Leu Arg Lys Thr Gly Lys Val Thr Val Arg Glu Thr Thr

85 90 95

ttg aag aga ctt gga gcc agc cat tct aaa tac ggt gtc gtt gac gaa 336

Leu Lys Arg Leu Gly Ala Ser His Ser Lys Tyr Gly Val Val Asp Glu
100 105 110

cac ttt gag gtg gcc aag tat gca ttg ttg gag acg ata aag gag gca 384

His Phe Glu Val Ala Lys Tyr Ala Leu Leu Glu Thr Ile Lys Glu Ala 115 120 125 gtg ccg gag atg tgg tca ccg gag atg aag gtg gct tgg ggt cag gct 432

Val Pro Glu Met Trp Ser Pro Glu Met Lys Val Ala Trp Gly Gln Ala 130 135 140

tat gat cac ctt gtt gct gcc att aaa gct gaa atg aat ctt tcc aac 480

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taa 483

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Val Val Lys Ser Trp Ser Val Met Lys Lys Asn Ser Ala Glu Leu Gly 20 25 30

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35 40 45

Met Phe Ser Phe Leu Arg Asp Ser Pro Ile Pro Ala Glu Gln Asn Pro 50 55 60

Lys Leu Lys Pro His Ala Met Ser Val Phe Val Met Cys Cys Glu Ser 65 70 75 80

Ala Val Gln Leu Arg Lys Thr Gly Lys Val Thr Val Arg Glu Thr Thr 85 90 95

Leu Lys Arg Leu Gly Ala Ser His Ser Lys Tyr Gly Val Val Asp Glu
100 105 110

His Phe Glu Val Ala Lys Tyr Ala Leu Leu Glu Thr Ile Lys Glu Ala 115 120 125

Val Pro Glu Met Trp Ser Pro Glu Met Lys Val Ala Trp Gly Gln Ala 130 135 140

Tyr Asp His Leu Val Ala Ala Ile Lys Ala Glu Met Asn Leu Ser Asn 145 150 155 160

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tcg tgg gag ata ctg aaa caa gac atc ccc aaa tac agc ctt cac ttc 96

Ser Trp Glu Ile Leu Lys Gln Asp Ile Pro Lys Tyr Ser Leu His Phe 20 25 30

ttc tca cag ata ctg gag ata gca cca gca gca aaa ggc ttg ttc tct 144

Phe Ser Gln Ile Leu Glu Ile Ala Pro Ala Ala Lys Gly Leu Phe Ser 35 40 45

ttc cta aga gac tca gat gaa gtc cct cac aac aat cct aaa ctc aaa 192

Phe Leu Arg Asp Ser Asp Glu Val Pro His Asn Asn Pro Lys Leu Lys
50 55 60

get cat get gtt aaa gte tte aag atg aca tgt gaa aca get ata cag 240

Ala His Ala Val Lys Val Phe Lys Met Thr Cys Glu Thr Ala Ile Gln 65 70 75 80

ctg agg gag gaa gga aag gtg gta gtg gct gac aca acc ctc caa tat 288

Leu Arg Glu Glu Gly Lys Val Val Ala Asp Thr Thr Leu Gln Tyr 85 90 95

tta ggc tca att cat ctc aaa agc ggc gtt att gac cct cac ttc gag 336

Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu
100 105 110

gtg gtg aaa gaa gct ttg cta agg aca ttg aaa gag ggg ttg ggg gag

384

Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu

115

120 -

125

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Lys Tyr Asn Glu Glu Val Glu Gly Ala Trp Ser Gln Ala Tyr Asp His 130 135 140

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Phe Ser Gln Ile Leu Glu Ile Ala Pro Ala Ala Lys Gly Leu Phe Ser 35 40 45

Phe Leu Arg Asp Ser Asp Glu Val Pro His Asn Asn Pro Lys Leu Lys
50 55 60

Ala His Ala Val Lys Val Phe Lys Met Thr Cys Glu Thr Ala Ile Gln 65 70 75 80

Leu Arg Glu Glu Gly Lys Val Val Ala Asp Thr Thr Leu Gln Tyr 85 90 95

Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu
100 105 110

Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu
115 120 125

Lys Tyr Asn Glu Glu Val Glu Gly Ala Trp Ser Gln Ala Tyr Asp His 130 135 140